IN THE CLAIMS

Please amend the claims as follows:

Claims 1-25 (Cancelled)

Claim 26 (Currently Amended): An isolated polynucleotide that encodes ~~a polypeptide which has transcription regulator LysR2 activity and which polypeptide is least 90% identical to~~ the polypeptide of SEQ ID NO: 2.

Claim 27 (Currently Amended): The isolated polynucleotide of Claim 26, which comprises nucleotides 232 to 1161 of SEQ ID NO: 1 ~~encodes a polypeptide which is at least 95% identical to SEQ ID NO: 2~~.

Claims 28-30 (Cancelled)

Claim 31 (Previously Presented): The isolated polynucleotide of Claim 26 which is DNA.

Claim 32 (Previously Presented): The isolated polynucleotide of Claim 26 which is RNA.

Claims 33-35 (Cancelled)

Claim 36 (Currently Amended): An isolated polynucleotide fragment of SEQ ID NO: 1 which ~~comprises~~ consists of at least 15 consecutive nucleotides of SEQ ID NO: 1.

Claim 37 (Currently Amended): The isolated polynucleotide fragment of Claim 36, which ~~comprises~~ consists of at least 15 consecutive nucleotides between nucleotides 232 to 1161 of SEQ ID NO: 1.

Claim 38 (Currently Amended): The isolated polynucleotide fragment of Claim 36 which comprises SEQ ID NO: ~~1~~ 3.

Claim 39 (Previously Presented): The isolated polynucleotide of Claim 36 which encodes the polypeptide of SEQ ID NO: 2.

Claim 40 (Currently Amended): An isolated polynucleotide fragment of the full complement of SEQ ID NO: 1 which ~~comprises~~ consists of at least 15 consecutive nucleotides of the full complement of SEQ ID NO: 1.

Claim 41 (Previously Presented): A vector comprising the polynucleotide of Claim 26.

Claims 42 (Currently Amended): A vector comprising the polynucleotide of Claim ~~30~~ 27.

Claim 43 (Currently Amended): A vector comprising the polynucleotide of Claim ~~33~~ 36.

Claim 44 (Currently Amended): A vector comprising the polynucleotide of Claim ~~36~~ 38.

Claim 45 (Currently Amended): A vector comprising the polynucleotide of Claim ~~38~~ 40.

Claim 46 (Previously Presented): Vector pCR2.1lysR2int.

Claim 47 (Previously Presented): A host cell comprising the polynucleotide of Claim 26.

Claims 48 (Currently Amended): A host cell comprising the polynucleotide of Claim ~~30~~ 27.

Claim 49 (Currently Amended): A host cell comprising the polynucleotide of Claim ~~33~~ 36.

Claim 50 (Previously Presented): A host cell comprising the polynucleotide of Claim 38.

Claim 51 (Currently Amended): An isolated coryneform bacterium, comprising eliminating the intracellular activity of the lysR2 gene product comprising the amino acid sequence of SEQ ID NO: 2 ~~which expresses a decreased amount of the product of the *lysR2* gene compared to the unmodified starting strain~~.

Claim 52 (Previously Presented): The isolated coryneform bacterium of Claim 51, wherein the *lysR2* gene has been eliminated.

Claim 53 (Currently Amended): The isolated coryneform bacterium of Claim 51, wherein the *lysR2* gene has been inactivated or in which expression of the lysR2 gene has been eliminated.

Claim 54 (Cancelled)

Claim 55 (Cancelled)

Claim 56 (Previously Presented): The isolated coryneform bacterium of Claim 51, which is of the genus *Corynebacterium* or *Brevibacterium*.

Claim 57 (Previously Presented): The isolated coryneform bacterium of Claim 51, which is selected from the group consisting of *Corynebacterium glutamicum, Corynebacterium acetoglutamicum, Corynebacterium acetoacidophilum, Corynebacterium melassecola, Corynebacterium themoaminogenes, Brevibacterium flavum, Brevibacterium lactofermentum*, and *Brevibacterium divaricatum*.

Claim 58 (Previously Presented): A process for making an L-amino acid comprising:

a) culturing the bacterium of Claim 51 in an medium suitable for the production of said L-amino acid by fermentation, and

b) recovering said L-amino acid from the culture medium or from the bacterial cells.

Claim 59 (Previously Presented): The process of Claim 58, wherein said amino acid is L-lysine.

Claim 60 (Previously Presented): The process of Claim 58, wherein said amino acid is L-valine.

Claim 61 (Previously Presented): The process of Claim 58, wherein in said bacterium the *lysR2* gene has been eliminated or inactivated.

Claim 62-63 (Cancelled)

Claim 64 (Previously Presented): The process of Claim 58, wherein said bacterium is from the genus *Corynebacterium* or *Brevibacterium*.

Claim 65 (Previously Presented): The process of Claim 58, wherein said bacterium is selected from the group consisting of *Corynebacterium glutamicum, Corynebacterium acetoglutamicum, Corynebacterium acetoacidophilum, Corynebacterium melassecola, Corynebacterium themoaminogenes, Brevibacterium flavum, Brevibacterium lactofermentum*, and *Brevibacterium divaricatum*.

Claim 66 (Currently Amended): The process of Claim 58, wherein said bacterium further comprises at least one gene whose expression is enhanced, ~~(~~compared to an unmodified starting strain~~)~~, selected from the group consisting of:

the *dapA* gene which codes for dihydrodipicolinate synthase,

the *eno* gene which codes for enolase,

the *zwf* gene which codes for the *zwf* gene product,

the *pyc* gene which codes for pyruvate carboxylase,

the *lysE* gene which codes for lysine export, and

the *lysC* gene which codes for a feed-back resistant aspartate kinase.

Claim 67 (Currently Amended): The process of Claim 58, wherein said bacterium further comprises at least one gene whose expression is attenuated, ~~(~~compared to an unmodified starting strain~~)~~, selected from the group consisting of:

the *pck* gene which codes for phosphoenol pyruvate carboxykinase,

the *pgi* gene which codes for glucose 6-phosphate isomerase,

the *poxB* gene which codes for pyruvate oxidase,

the *hom* gene which codes for homoserine dehydrogenase

the *thrB* gene which codes for homoserine kinase, and

the *panD* gene which codes for aspartate decarboxylase.

Claim 68 (New): The isolated coryneform bacterium according to Claim 51, wherein elimination is achieved by one or more methods of mutagenesis of the polynucleotide encoding the polypeptide having the amino acid sequence of SEQ ID NO: 2 selected from the group consisting of deletion mutagenesis of two or more codons, insertion or deletion mutagenesis of at least one nucleotide and transition or transversion mutagenesis of at least one nucleotide with incorporation of a nonsense mutation.